

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2004, 13:51:35 ; Search time 75.7714 Seconds
(without alignments)
1136.247 Million cell updates/sec

Title: US-10-630-406-8

Perfect score: 1244

Sequence: 1 MEAPQAQLFLLLWLPLDTTG.....EVTHQGLSSPVTKSFNRGEC 240

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04: *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1244	100.0	240	8	ADJ65029 Plasmid p
2	1133	91.1	240	2	AAY50161 Human res
3	1128.5	90.7	241	2	AAR28809 Vector pM
4	1122	90.2	240	5	AAE27927 Human CC4
5	1122	90.2	240	6	ABB82836 Antibody
6	1099	88.3	240	4	AAU00815 Human Imm
7	1075	86.4	244	3	AAY96305 Human IGF
8	1066	85.7	220	8	ADK52334 Human ant
9	1063	85.5	238	8	ADL23055 Humanised
10	1061	85.3	220	8	ADK52386 Human ant
11	1059	85.1	240	2	AAY50156 Chimeric
12	1057	85.0	220	8	ADK52362 Human ant
13	1056	84.9	220	8	ADK52314 Human ant
14	1053	84.6	238	6	ADA47330 TRX1 ligh
15	1053	84.6	238	6	ADA47332 TRX1 ligh
16	1053	84.6	238	8	ADP88450 Antibody
17	1053	84.6	238	8	ADP88426 Antibody
18	1052.5	84.6	235	3	AAY93702 The kappa
19	1052.5	84.6	235	3	AAY93729 The kappa
20	1052.5	84.6	235	6	AAE35884 Human 4.1
21	1051	84.5	234	3	AAY92239 Human bon
22	1047	84.2	220	8	ADK52298 Human ant
23	1043.5	83.9	235	6	ABP71366 Anti-OPGL
24	1043	83.8	238	6	ADA47339 TRX1 ligh
25	1043	83.8	238	6	ADA47338 TRX1 ligh

26	1043	83.8	238	8	ADP88434	Adp88434 Antibody
27	1043	83.8	238	8	ADP88442	Adp88442 Antibody
28	1041	83.7	220	2	AAY08601	Aay08601 JP1112785
29	1040.5	83.6	233	3	AAY93704	Aay93704 The kappa
30	1040.5	83.6	233	3	AAY93731	Aay93731 The kappa
31	1040.5	83.6	233	6	AAE35886	Aae35886 Human 4.8
32	1037	83.4	234	3	AAY93733	Aay93733 The kappa
33	1037	83.4	234	3	AAY93708	Aay93708 The kappa
34	1037	83.4	234	6	AAE35888	Aae35888 Human 6.1
35	1036	83.3	234	7	ADE28481	Ade28481 Human ant
36	1036	83.3	236	5	AAU74299	Aau74299 Anti-huma
37	1032.5	83.0	239	8	ADK70470	Adk70470 Respirato
38	1032	83.0	234	2	AAR52951	Aar52951 Human ant
39	1031.5	82.9	235	8	ADM41573	Adm41573 Anti-inte
40	1030	82.8	236	4	AAG71272	Aag71272 Human gen
41	1030	82.8	236	5	ABG63490	Abg63490 Human alb
42	1030	82.8	236	8	ADL76755	Adl76755 Albumin f
43	1029.5	82.8	237	2	AAW73873	Aaw73873 Human ant
44	1028	82.6	236	5	AAU74301	Aau74301 Anti-huma
45	1027	82.6	242	4	AAU80338	Aau80338 Human mil

ALIGNMENTS

RESULT 1

ADJ65029 ADJ65029 standard; protein; 240 AA.

XX ADJ65029;

XX 06-MAY-2004 (first entry)

DE Plasmid pD16-H39E3.L1 light chain antibody amino acid sequence SEQ:8.

XX humanised antibody; human 4-1BB; human 4-1BB ligand; cancer; cytostatic;

KW gene therapy; antibody; plasmid; pD16-H39E3.L1.

XX Synthetic.

PN WO2004010947-A2.

XX 05-FEB-2004.

PF 30-JUL-2003; 2003WO-US023735.

PR 30-JUL-2002; 2002US-0399646P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX Jure-Kunkel M, Ganguly S, Abraham R, Hollenbaugh DL, Rillema J;

PI Thorne B, Shuford WW, Mittler RS;

XX WPI; 2004-143726/14.

DR N-PSDB; ADJ65027.

XX New humanized antibody that binds to human 4-1BB and allows binding of human 4-1BB to a human 4-1BB ligand, useful for preparing a composition for treating cancer.

PS Claim 4; SEQ ID NO 8; 78pp; English.

XX The present invention describes a humanised antibody (I) that binds to human 4-1BB and allows binding of human 4-1BB to a human 4-1BB ligand. Also described: (1) a pharmaceutical composition comprising the antibody (I) and a carrier; (2) treating cancer in a subject; and (3) an isolated polynucleotide comprising nucleotides 693-2072 of the 7033-base pairs (bp) sequence (SEQ ID NO: 3, ADJ65024) or nucleotides 633-1034 or 1409-1726 of the 8874-bp sequence (SEQ ID NO: 6, ADJ65027). (I) has cytostatic activity, and can be used in gene therapy. The humanised antibody (I) can be used for preparing a composition for treating cancer. The present sequence represents the plasmid pD16-H39E3.L1 light chain antibody amino acid sequence, which is used in an example from the present invention.

XX SQ Sequence 240 AA;
Query Match 100.0%; Score 1244; DB 8; Length 240;
Best Local Similarity 100.0%; Pred. No. 3.9e-68;
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEAPAQLLFLLLLWLPDITGDIVMTQSPDSLAVSLGERATINCKSSQSLSSGNQKNYLA 60
Db 1 MEAPAQLLFLLLLWLPDITGDIVMTQSPDSLAVSLGERATINCKSSQSLSSGNQKNYLA 60
QY 61 WYQOKPGQPPKLLIYVASTROSGVDPDRFSGSGSGTDTFTLTSSLOAEDVAVYYCLOYDRY 120
Db 61 WYQOKPGQPPKLLIYVASTROSGVDPDRFSGSGSGTDTFTLTSSLOAEDVAVYYCLOYDRY 120
QY 121 PFTFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 180
Db 121 PFTFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 180
QY 181 QSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db 181 QSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 240

RESULT 2

AAY50161

ID AAY50161 standard; protein; 240 AA.

XX AC AAY50161;

XX DT 17-OCT-2003 (revised)

XX DT 31-JAN-2000 (first entry)

XX DE Human reshaped F19 antibody light chain (version a).

XX KW Antibody; monoclonal; F19; fibrinogen activation protein alpha; FAP;

XX KW humanisation; complementarity determining region; CDR; CDR grafting;

XX KW reshaped; reactive stroma; fibroblast; epithelial cancer; diagnosis;

XX KW immune response; framework sequence; constant region; variable region;

XX KW producibility; treatment; cancer; colorectal; lung; breast; head; neck;

XX KW ovarian; lung; bladder; pancreatic; metastasis; detection; wound healing;

XX KW skin inflammation; tumour; immunogenicity; chimeric; light chain.

XX OS Mus sp.

XX OS Homo sapiens.

XX OS Chimeric.

XX FH Key

XX FT Peptide

XX FT Protein

XX FT Region

XX FT Region

XX FT Region

XX FT Region

XX FT Region

XX FT Region

XX FT Region

XX FT Region

XX FT Region

XX FT Region

XX FT Region

XX FT Region

XX FT Region

XX FT Region

XX FT Region

XX FT Region

XX FT Region

XX FT Region

XX FT Region

XX FT Region

XX FT Region

XX FT Region

XX FT Region

XX FT Region

XX FT Region

XX FT Region

XX FT Region

XX FT Region

XX FT Region

XX FT Region

XX PI Park JE, Garin-Chesa P, Bamberger U, Leger O, Saldanha J;
PI Rettig WJ;
XX WPI; 1999-621833/54.
DR N-PSDB; AAZ32784.
XX
PT New antibody protein, useful for treating cancer and for imaging presence
PT of activated stromal fibroblasts in healing wound or inflamed skin.
XX
PS Example 3; Fig 30; 143pp; English.
XX
CC This sequence represents the light chain (version a) of a reshaped human
CC F19 antibody. F19 (ATCC Accession number HB 8269) is a murine monoclonal
CC antibody against fibroblast activation protein alpha (FAP). FAP is a cell
CC surface molecule of reactive stromal fibroblasts, and its induction is a
CC highly consistent molecular trait of the reactive stroma of many types of
CC epithelial cancer. Although F19 may be useful in vitro, e.g., for
CC diagnosis, its applications for in vivo use in humans are problematic as
CC it elicits a human anti-mouse response which reduces the efficacy of the
CC antibody in patients and impairs continued administration. The novel
CC human reshaped F19 was humanised by grafting the murine complementarity
CC determining regions (CDRs) of F19 onto human variable region framework
CC sequences, and then joining these "reshaped human" variable regions to
CC human constant regions. These modifications also result in the improved
CC human constant regions. The entire variable regions of F19 joined to
CC chimeric antibody having the entire variable regions of F19 joined to
CC human constant regions. The human reshaped F19 antibody has low
CC immunogenicity for humans and is useful for treating cancers e.g.,
CC colorectal cancers, non-small cell lung cancers, breast cancers, head and
CC neck cancers, ovarian cancers, lung cancers, bladder cancers, pancreatic
CC cancers and metastatic cancers. It is also useful for the detection of
CC activated stromal fibroblasts in a healing wound, inflamed skin or a
CC tumour in a human patient. (Updated on 17-OCT-2003 to standardise OS
CC field)
XX SQ Sequence 240 AA;

Query Match 91.1%; Score 1133; DB 2; Length 240;
Best Local Similarity 91.2%; Pred. No. 2.1e-61;
Matches 219; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 1 MEAPAQLLFLLLLWLPDITGDIVMTQSPDSLAVSLGERATINCKSSQSLSSGNQKNYLA 60
Db 1 METDTLLWVLLWVPGSSGDIVMTQSPDSLAVSLGERATINCKSSQSLSSGNQKNYLA 60
QY 61 WYQOKPGQPPKLLIYVASTROSGVDPDRFSGSGSGTDTFTLTSSLOAEDVAVYYCLOYDRY 120
Db 61 WYQOKPGQPPKLLIYVASTROSGVDPDRFSGSGSGTDTFTLTSSLOAEDVAVYYCLOYDRY 120
QY 121 PFTFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 180
Db 121 PLTFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 180
QY 181 QSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db 181 QSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 240

RESULT 3

AAR28809

ID AAR28809 standard; protein; 241 AA.

XX AC AAR28809;

XX DT 25-MAR-2003 (revised)

XX DT 02-APR-1993 (first entry)

XX DE Vector pMDR1007.

XX KW Plasmid; pMDR1006; pSAB132; vector; pMDR1007; pMDR985; AatII; EcoRV;

XX KW pMDR986; BglII; pMDR1003; JA221(Iq); E. coli; ampicillin resistance;

XX KW NotI; dephosphorylate; calf; alkaline phosphatase; low temperature;

XX KW

XX KW

XX KW

XX KW

XX KW

XX KW

XX KW

XX KW

QY 61 KGLEWVADIKNDGSYNYAPSLNRTTISRDNKNSLYLQMNLSRAEDTAVYYCARELT 120
Db 61 KGLEWVADIKNDGSYNYAPSLNRTTISRDNKNSLYLQMNLSRAEDTAVYYCARELT 120
QY 121 GTWQGTMTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSNWGALT 180
Db 121 GTWQGTMTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSNWGALT 180
QY 181 SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGKTYYTCNVDPKPSNTKVDKRVESKYGPPCP 240
Db 181 SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGKTYYTCNVDPKPSNTKVDKRVESKYGPPCP 240
QY 241 PCPAPEFLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNA 300
Db 241 PCPAPEFLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNA 300
QY 301 KTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQ 360
Db 301 KTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQ 360
QY 361 VYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY 420
Db 361 VYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY 420
QY 421 SRTLVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLGLK 460
Db 421 SRTLVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLGLK 460

RESULT 2

US-10-663-244-163
; Sequence 163, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; PRIOR FILING DATE: 2003-09-15
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 163
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-163

Query Match 92.5%; Score 2269; DB 16; Length 462;
Best Local Similarity 93.1%; Pred. No. 1.3e-136;
Matches 433; Conservative 7; Mismatches 17; Indels 8; Gaps 2;

QY 1 MDWTRILFLVAAATGAHSEVQLVESGGGLVQPGGSLRLSCAASGFTFSDYWMWVRQAP 60
Db 1 MGWSCIILFLVATATGAHSEVQLLESGLLVQPGGSLRLSCAASGFTFSDYWMWVRQAP 60
QY 61 KGLEWVADIKNDGSYNYAPSLNRTTISRDNKNSLYLQMNLSRAEDTAVYYCARELT 120
Db 61 KGLEWVSSIGPSGGLTNYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAR --- 117
QY 121 GT-----WGQGTMTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSNW 175
Db 118 GTRVTNWGQGTTLTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSNW 177
QY 176 SGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGKTYYTCNVDPKPSNTKVDKRVESKY 235

Db 178 SGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGKTYYTCNVDPKPSNTKVDKRVESKY 237
QY 236 GPPCPPCPAPEFLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGV 295
Db 238 GPPCPSCPAPEFLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGV 297
QY 296 EVHNAKTPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQ 355
Db 298 EVHNAKTPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQ 357
QY 356 PREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 415
Db 358 PREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 417
QY 416 SFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLGLK 460
Db 418 SFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLGLK 462

RESULT 3

US-10-663-244-160
; Sequence 160, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 160
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-160

Query Match 92.4%; Score 2268.5; DB 16; Length 463;
Best Local Similarity 92.7%; Pred. No. 1.4e-136;
Matches 429; Conservative 12; Mismatches 19; Indels 3; Gaps 1;

QY 1 MDWTRILFLVAAATGAHSEVQLVESGGGLVQPGGSLRLSCAASGFTFSDYWMWVRQAP 60
Db 1 MGWSCIILFLVATATGAHSEVQLLESGLLVQPGGSLRLSCAASGFTFSDYWMWVRQAP 60
QY 61 KGLEWVADIKNDGSYNYAPSLNRTTISRDNKNSLYLQMNLSRAEDTAVYYCAR --- 117
Db 61 KGLEWVSSIVSSGGFTKYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARGWS 120
QY 118 ELTGTWQGTMTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSNWG 177
Db 121 SQPAIWGQGSLLTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSNWG 180
QY 178 ALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGKTYYTCNVDPKPSNTKVDKRVESKYGP 237
Db 181 ALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGKTYYTCNVDPKPSNTKVDKRVESKYGP 240
QY 238 PCPPCPAPEFLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEV 297
Db 241 PCPPCPAPEFLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEV 300
QY 298 HNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPR 357
Db 301 HNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPR 360